

## SEQUENCE LISTING

<110> West, James W.  
 Brandt, Cameron S.  
 Jaspers, Stephen R.

<120> Production of Homotrimeric Fusion  
 Proteins

<130> 02-17

<150> 60/417,801

<151> 2002-10-11

<160> 22

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> C-myc tag.

<400> 1  
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
 1 5 10

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Hemagglutinin A epitope tag

<400> 2  
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
 1 5

<210> 3

<211> 1377

<212> DNA

<213> Human

<220>

<221> CDS

<222> (14)...(892)

<400> 3  
 agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg 49  
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg  
 1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97  
 Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly  
 15 20 25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145

•

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg 912

Pro Ala Gln Glu Gly Gly Pro Gly Ala  
285 290

aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972  
gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032  
gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092  
ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152  
gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggaggtc 1212  
ggggcactct gagtcccagt tcccagtgca gctgtaggtc gtcacacacgt aaccacacgt 1272  
gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332  
aaacctttgg cagctgcct tcctcaaaaa aaaaaaaaaa aaaaa 1377

<210> 4  
<211> 293  
<212> PRT  
<213> Human

<400> 4

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
1 5 10 15  
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg  
20 25 30  
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
35 40 45  
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
50 55 60  
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
65 70 75 80  
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
85 90 95  
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
100 105 110  
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
115 120 125  
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
130 135 140  
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
145 150 155 160  
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
165 170 175  
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
180 185 190  
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
195 200 205  
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
210 215 220  
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
225 230 235 240  
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
245 250 255  
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
260 265 270  
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu  
275 280 285  
Gly Gly Pro Gly Ala  
290

<210> 5  
<211> 21

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 5  
 gggcctccag gccaccagg t 21  
  
 <210> 6  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 6  
 tcacattgga gccactagga a 21  
  
 <210> 7  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 7  
 acaggtgtcc aggggaattca tataggccgg ccaccatgga tgcaatgaag agaggg 56  
  
 <210> 8  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 8  
 accctcaggc atcgaaccgc aaccgaacc ggatcc 36  
  
 <210> 9  
 <211> 118  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 9  
 gatcgatcc atggccgaaa ctgatacctaa aacagttcaa gaccttacca gcgtagtcca 60  
 gacgctcctg caagagatcg aagataagtt tcagactatg agcgaccaaa tcattgag 118  
  
 <210> 10  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer

<400> 10  
 agaatgcatg acatgagctc caggatagat gaccttgaga aaaatatagc agatttaatg 60  
 acgcaagctg gtgtggaaga gttggaagga agtggttcta 100

<210> 11  
 <211> 110  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 11  
 gatctagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata 60  
 tttttctcaa ggcatctat cctggagctc atgtcatcga ttctctcaat 110

<210> 12  
 <211> 108  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 12  
 gatttggtcg ctcatagtct gaaacttata ttgcatctct tgcaggagcg tctggactac 60  
 gctggtaagg tcttgaactg ttttaggata agtttcggcc atggatcc 108

<210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 13  
 cacacgtacg aagatggatg caatgaagag agg 33

<210> 14  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 14  
 ggttagatct cgaacccgaa cccgaaccgg 30

<210> 15  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 15  
 ctagaaataa ttttgtttta ctttaagaag gagatatata tatggctatg agatcctgcc 60  
 cc 62

<210> 16  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 16  
 tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgatgg tgatggatgat 60  
 ggcc 64

<210> 17  
 <211> 516  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TACI-HSBP fragment

<400> 17  
 atggctatga gatcctgccc cgaagagcag tactgggcatc ctctgctggg tacctgcatg 60  
 tcctgcaaaa ccatttgcaa ccatcagagc cagcgacact gtgcagcctt ctgcagggtca 120  
 ctcagctgcc gcaaggagca aggcaagttc tatgaccatc tcctgaggga ctgcatcagc 180  
 tgtgcctcca tctgtggaca gcaccctaag caatgtgcat acttctgtga gaacaagctc 240  
 aggagcggat ccggttcggg ttcgggttcg agatccatgg ccgaaactga tcctaaaaca 300  
 gttcaagacc ttaccagcgt agtccagacg ctctgcaag agatgcaaga taagtttcag 360  
 actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgacctt 420  
 gagaaaaata tagcagattt aatgacgcaa gctgggtgtgg aagagttgga aggaagtgg 480  
 tctagatccg gtggccatca ccatcaccat cactga 516

<210> 18  
 <211> 171  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TACI-HSBP fragment

<400> 18  
 Met Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu  
 1 5 10 15  
 Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg  
 20 25 30  
 Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly  
 35 40 45  
 Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile  
 50 55 60  
 Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu  
 65 70 75 80  
 Arg Ser Gly Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr  
 85 90 95  
 Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu  
 100 105 110  
 Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp Gln Ile Ile Glu  
 115 120 125  
 Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu Glu Lys Asn Ile  
 130 135 140  
 Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu Glu Gly Ser Gly  
 145 150 155 160  
 Ser Arg Ser Gly Gly His His His His His His  
 165 170

<210> 19  
 <211> 480  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> NC-1 fragment

<221> CDS  
 <222> (1)...(480)

```

<400> 19
atg cct gag ggt ttt ata aag gca ggc caa agg ccc agt ctt tct ggg      48
Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
  1              5              10              15

acc cct ctt gtt agt gcc aac cag cgg gta aca gga atg cct gtg tct      96
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
              20              25              30

gct ttt act gtt att ctc tcc aaa gct tac cca gca ata gga act ccc      144
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
              35              40              45

ata cca ttt gat aaa att ttg tat aac agg caa cag cat tat gac cca      192
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
              50              55              60

agg act gga atc ttt act tgt cag ata cca gga ata tac tat ttt tca      240
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
              65              70              75              80

tac cac gtg cat gtg aaa ggg act cat gtt tgg gta ggc ctg tat aag      288
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
              85              90              95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac      336
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
              100              105              110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac      384
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
              115              120              125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc      432
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
              130              135              140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg      480
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
145              150              155              160

```

<210> 20  
 <211> 160  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> NC-1 fragment

<400> 20

```

Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1      5      10      15
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
      20      25      30
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
      35      40      45
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
      50      55      60
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
      65      70      75      80
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
      85      90      95
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
      100      105      110
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
      115      120      125
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
      130      135      140
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
      145      150      155      160

```

```

<210> 21
<211> 195
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> HSBP-1 fragment

```

```

<221> CDS
<222> (1)...(195)

```

```

<400> 21
atg gcc gaa act gat cct aaa aca gtt caa gac ctt acc agc gta gtc      48
Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val
 1      5      10      15

cag acg ctc ctg caa gag atg caa gat aag ttt cag act atg agc gac      96
Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp
      20      25      30

caa atc att gag aga atc gat gac atg agc tcc agg ata gat gac ctt      144
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
      35      40      45

gag aaa aat ata gca gat tta atg acg caa gct ggt gtg gaa gag ttg      192
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu
      50      55      60

gaa      195

```

```

<210> 22
<211> 65
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> HSBP-1 fragment

```

<400> 22  
 Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val  
 1 5 10 15  
 Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp  
 20 25 30  
 Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu  
 35 40 45  
 Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu  
 50 55 60  
 Glu  
 65